

10/524983

21078WO.ST25.txt

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<213> *Aspergillus niger*

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<213> *Aspergillus niger*

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<212> DNA

<213> *Aspergillus niger*

<220>

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<222> (1)..(1743)

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gct act gta cga aat ggc acc tac tat ggt ctc cat aac cag cac tat	144
Ala Thr Val Arg Asn Gly Thr Tyr Tyr Gly Leu His Asn Gln His Tyr	
35 40 45	
aat caa gac ctc ttt ctc ggt att cca tat gca cag caa cct att ggt	192
Asn Gln Asp Leu Phe Leu Gly Ile Pro Tyr Ala Gln Gln Pro Ile Gly	
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gac ctt cgc ttg cgg acc cca cga tca atg aac acc tcc tgg cca gta	240
Asp Leu Arg Leu Arg Thr Pro Arg Ser Met Asn Thr Ser Trp Pro Val	
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cca aga aat gca aca gaa tat tca ccc gca tgt gtt gga ttt aat cag	288
Pro Arg Asn Ala Thr Glu Tyr Ser Pro Ala Cys Val Gly Phe Asn Gln	
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aca gag ggt gct tcc gaa gcc tgc ctt act ctc aat gtc gtc cgc ccg	336
Thr Glu Gly Ala Ser Glu Ala Cys Leu Thr Leu Asn Val Val Arg Pro	
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gca agc atc gct ctt tct gaa agt ctt ccc gtt gct gtc tgg att cat	384
Ala Ser Ile Ala Leu Ser Glu Ser Leu Pro Val Ala Val Trp Ile His	
115 120 125	

21078WO.ST25.txt

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tcc ttc atc gtt gat cag tca gtc caa atg gaa aag ccc gtt atc gca	480
Ser Phe Ile Val Asp Gln Ser Val Gln Met Glu Lys Pro Val Ile Ala	
145 150 155 160	
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Val Ser Leu Asn Tyr Arg Leu Gln Cys Trp Gly Phe Met Trp Ser Lys	
165 170 175	
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Glu Met Lys Glu Ala Gly Val Gly Asn Leu Gly Leu Arg Asp Gln Arg	
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Pro Ala Gln Val Thr Ile Trp Gly Glu Ser Ala Gly Ala Asn Ser Val	
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Ala Ala Ile Ser Glu Ser Gly Ala Pro Ser Val Tyr Gln Arg Tyr Pro	
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Thr Pro Ala Glu Trp Gln Pro Tyr Tyr Asp Gly Ile Val Asn Ala Ser	
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Phe Val Lys Val Pro Tyr Leu Ile Gly Ala Asn Ala Asp Glu Gly Thr	
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Leu Tyr Pro Asp Ile Pro Gln Ile Gly Ile Pro Ala Ile Met Val Gly			
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Arg Pro Pro Ser Gly Tyr Gly Asn Gln Tyr Lys Arg Val Ala Ala Phe			
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Gln Gly Asp Val Asn Ile His Ala Ala Arg Arg Leu Thr Ser Gln Ile			
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Trp Ser Ser Arg Asn Ile Ser Val Tyr Ser Tyr Met Phe Asp Val Ile			
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Met Ser Lys Ile Met Ser Arg Met Trp Val Ser Phe Val Thr Thr Leu			
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Asp Pro Asn His Ser Gly Gly Met Val Pro His Pro Ile Pro Met Ile			
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<211> 580

<212> PRT

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<400> 6

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Glu Met Lys Glu Ala Gly Val Gly Asn Leu Gly Leu Arg Asp Gln Arg
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21078WO.ST25.txt

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 355 360 365
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 370 375 380
 Leu Tyr Pro Asp Ile Pro Gln Ile Gly Ile Pro Ala Ile Met Val Gly
 385 390 395 400
 Arg Pro Pro Ser Gly Tyr Gly Asn Gln Tyr Lys Arg Val Ala Ala Phe
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<213> Aspergillus niger

21078WO.ST25.txt

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<211> 1623

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(1623)

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Arg Ala Ser Ile Gly Leu Glu Thr Tyr Arg Tyr Tyr Trp Ala Gly Asn
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ttc tcc aat atc agt ccc gta ccg tgg cta gga gca ttc cac tgg acc      1344
Phe Ser Asn Ile Ser Pro Val Pro Trp Leu Gly Ala Phe His Trp Thr
              435              440              445
gac ctg ctg atg atc ttc ggt acg tat aat ctg gac gtc ggc gag atc      1392
Asp Leu Leu Met Ile Phe Gly Thr Tyr Asn Leu Asp Val Gly Glu Ile
              450              455              460
tcg cag ttg gaa gtc gac acc tct gcc acg atg caa gat tat cta ctc      1440
Ser Gln Leu Glu Val Asp Thr Ser Ala Thr Met Gln Asp Tyr Leu Leu
465              470              475              480
gcc ttt ctg aag gac tca tca acc gtc agc gag acg gtc gga tgg ccg      1488
Ala Phe Leu Lys Asp Ser Ser Thr Val Ser Glu Thr Val Gly Trp Pro
              485              490              495
tta tat ctg ggc aac gag acc aac gga gga ctc atc ctg gag ttc ggt      1536
Leu Tyr Leu Gly Asn Glu Thr Asn Gly Gly Leu Ile Leu Glu Phe Gly
              500              505              510
aac ggc aca gca gtg cgg acc atc aca ggt gac tgg ctc gac gcg gga      1584
Asn Gly Thr Ala Val Arg Thr Ile Thr Gly Asp Trp Leu Asp Ala Gly
              515              520              525
tgt ttc aat tca tct atc cca ttc aga atc tgg ggg tag      1623
Cys Phe Asn Ser Ser Ile Pro Phe Arg Ile Trp Gly
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<210> 9

<211> 540

<212> PRT

<213> *Aspergillus niger*

<400> 9

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Arg Thr Leu Ser Asn Trp Ser Asn Leu Thr Val Glu Thr Arg Thr Gly
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 85 90 95
 Tyr Gly Pro Ala Cys Pro Gln Tyr Val Pro Ala Glu Ser Asp Phe Trp
 100 105 110
 Asn Glu Tyr Glu Pro Glu Asn Leu Leu Leu Asn Val Gly Glu Arg Leu
 115 120 125
 Asn Gln Gly Ser Thr Ala Trp Ser Ser Ser Glu Asp Cys Leu Ser Leu
 130 135 140
 Ala Val Trp Thr Pro Ser Tyr Ala Asn Glu Thr Ser Lys Leu Pro Val
 145 150 155 160
 Ala Leu Phe Val Thr Gly Gly Gly Gly Ile Thr Gly Gly Ile Asn Ile
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 Pro Ser Gln Leu Pro Ser Ala Trp Val Ser Arg Ser Gln Glu His Ile
 180 185 190
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 195 200 205
 Arg Ala Leu Asn Asp Thr Ser Leu Thr Leu Met Asp Val Arg Ala Ala
 210 215 220
 Val Glu Trp Val Tyr Glu Asn Ile Glu Ala Phe Gly Gly Asn Pro Glu
 225 230 235 240
 Asn Ile Met Val Arg Leu Gln Val Ser Ser His Met Thr Arg Ala Asn
 245 250 255
 Ser Lys Gln Leu Trp Gly Gln Ser Gln Gly Ala Leu Leu Thr His Leu
 260 265 270
 Tyr Thr Leu Ala Trp Pro Glu Glu Pro Leu Ala Ala Lys Phe Gly Val
 275 280 285
 Ile Ser Gln Gly Ala Ser Ala Thr Leu Asn Leu Ser Thr Thr Pro Asp
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 Val Tyr Gln Asp Phe Asp Ile Val Ala Lys Gly Leu Gly Cys Asn Tyr
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 Gly Asp Asp Ala Glu Ala Glu Leu Glu Cys Met Arg Gly Ile Ser Trp
 325 330 335
 Val Gln Ile Glu Glu Tyr Ile Asn Arg Tyr Asn Ser Ser Pro Ser Ile
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 Ala Phe Thr Asn Tyr Ile Pro Asp Glu Lys Tyr Ile Phe Ser Asp Glu
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 Arg Gln Arg Tyr Leu Glu Arg Lys Val Ala Arg Gly Pro Ser Ile Arg
 370 375 380
 Ser Asp Thr Ala Arg Glu Phe Pro Ser Thr Asn Thr Thr Ser Val Asn
 385 390 395 400

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Ile Glu Glu Gly Glu Ser Asp Cys Leu Ala Val Thr Asp Leu Ala Leu
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 Arg Ala Ser Ile Gly Leu Glu Thr Tyr Arg Tyr Tyr Trp Ala Gly Asn
 420 425 430
 Phe Ser Asn Ile Ser Pro Val Pro Trp Leu Gly Ala Phe His Trp Thr
 435 440 445
 Asp Leu Leu Met Ile Phe Gly Thr Tyr Asn Leu Asp Val Gly Glu Ile
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 Ser Gln Leu Glu Val Asp Thr Ser Ala Thr Met Gln Asp Tyr Leu Leu
 465 470 475 480
 Ala Phe Leu Lys Asp Ser Ser Thr Val Ser Glu Thr Val Gly Trp Pro
 485 490 495
 Leu Tyr Leu Gly Asn Glu Thr Asn Gly Gly Leu Ile Leu Glu Phe Gly
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<211> 3235

<212> DNA

<213> *Aspergillus niger*

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<210> 11

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<212> DNA

<213> *Aspergillus niger*

<220>

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Trp Ala Thr Pro Val Gln Arg Asp Ala Ala Pro Thr Val Thr Ile Ala	
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cat cca tcg gcc acc gtc att gga aaa tct ggc aat gtc gag agc ttc	144
His Pro Ser Ala Thr Val Ile Gly Lys Ser Gly Asn Val Glu Ser Phe	
35 40 45	
aac aat att ccc ttt gcg cag gcc ccc aca ggc tcg ctg cgt ctg aag	192
Asn Asn Ile Pro Phe Ala Gln Ala Pro Thr Gly Ser Leu Arg Leu Lys	
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ccc cca caa ccc ttg gaa act gcc ctc ggc act gtt cag gcc aca gga	240
Pro Pro Gln Pro Leu Glu Thr Ala Leu Gly Thr Val Gln Ala Thr Gly	
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gcc tcg caa tcg tgt ccg cag atg tac ttc acc acg gat gag agc gaa	288
Ala Ser Gln Ser Cys Pro Gln Met Tyr Phe Thr Thr Asp Glu Ser Glu	
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Phe Pro Thr Ser Val Ile Gly Leu Leu Ala Asp Leu Pro Leu Val Gln	
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Ser Ala Thr Asn Ala Leu Glu Asp Cys Leu Asn Ile Asp Ile Arg Arg	
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ccg gcc ggg acc acc gcg gac tcg aag ctg cct gtg ctg gtc tgg atc	432
Pro Ala Gly Thr Thr Ala Asp Ser Lys Leu Pro Val Leu Val Trp Ile	
130 135 140	
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Phe Gly Gly Gly Phe Glu Leu Gly Ser Lys Ala Met Tyr Asp Gly Thr	
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Thr Met Val Ser Ser Ser Ile Asp Lys Asn Met Pro Ile Val Phe Val	
165 170 175	
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Ala Met Asn Tyr Arg Val Gly Gly Phe Gly Phe Leu Pro Gly Lys Glu	
180 185 190	
atc ctg gag gac ggg tcc gcg aac cta ggg ctc ctg gac caa cgc ctt	624
Ile Leu Glu Asp Gly Ser Ala Asn Leu Gly Leu Leu Asp Gln Arg Leu	
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gcc ctg cag tgg gtt gcc gac aac atc gag gcc ttt ggt gga gac ccg	672

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Ala Leu Gln Trp Val	Ala Asp Asn Ile Glu Ala Phe Gly Gly Asp Pro	
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Asp Lys Val Thr Ile Trp Gly Glu Ser Ala Gly Ala Ile Ser Val Phe		
225	230	235
gat cag atg atc ttg tac gac gga aac atc act tac aag gat aag ccc		768
Asp Gln Met Ile Leu Tyr Asp Gly Asn Ile Thr Tyr Lys Asp Lys Pro		
245	250	255
ttg ttc cgg ggg gcc atc atg gac tcc ggt agt gtt gtt ccc gca gac		816
Leu Phe Arg Gly Ala Ile Met Asp Ser Gly Ser Val Val Pro Ala Asp		
260	265	270
ccc gtc gat ggg gtc aag gga cag caa gta tat gat gcg gta gtg gaa		864
Pro Val Asp Gly Val Lys Gly Gln Gln Val Tyr Asp Ala Val Val Glu		
275	280	285
tct gca ggc tgt tcc tct tct aac gac acc cta gct tgt ctg cgt gaa		912
Ser Ala Gly Cys Ser Ser Ser Asn Asp Thr Leu Ala Cys Leu Arg Glu		
290	295	300
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Leu Asp Tyr Thr Asp Phe Leu Asn Ala Ala Asn Ser Val Pro Gly Ile		
305	310	315
tta agc tac cat tct gtg gcg tta tca tat gtg cct cga ccg gac ggg		1008
Leu Ser Tyr His Ser Val Ala Leu Ser Tyr Val Pro Arg Pro Asp Gly		
325	330	335
acg gcg ttg tcg gca tca ccg gac gtt ttg ggc aaa gca ggg aaa tat		1056
Thr Ala Leu Ser Ala Ser Pro Asp Val Leu Gly Lys Ala Gly Lys Tyr		
340	345	350
gct cgg gtc ccg ttc atc gtg ggc gac caa gag gat gag ggg acc tta		1104
Ala Arg Val Pro Phe Ile Val Gly Asp Gln Glu Asp Glu Gly Thr Leu		
355	360	365
ttc gcc ttg ttt cag tcc aac att acg acg atc gac gag gtg gtc gac		1152
Phe Ala Leu Phe Gln Ser Asn Ile Thr Thr Ile Asp Glu Val Val Asp		
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tac ctg gcc tca tac ttc ttc tat gac gct agc cga gag cag ctt gaa		1200
Tyr Leu Ala Ser Tyr Phe Phe Tyr Asp Ala Ser Arg Glu Gln Leu Glu		
385	390	395
gaa cta gtg gcc ctg tac cca gac acc acc acg tac ggg tct ccg ttc		1248
Glu Leu Val Ala Leu Tyr Pro Asp Thr Thr Thr Tyr Gly Ser Pro Phe		
405	410	415
agg aca ggc gcg gcc aac aac tgg tat ccg caa ttt aag cga ttg gcc		1296
Arg Thr Gly Ala Ala Asn Asn Trp Tyr Pro Gln Phe Lys Arg Leu Ala		
420	425	430
gcc att ctc ggc gac ttg gtc ttc acc att acc cgg cgg gca ttc ctc		1344
Ala Ile Leu Gly Asp Leu Val Phe Thr Ile Thr Arg Arg Ala Phe Leu		
435	440	445

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gcg acc tat gac tat ggc acc cca gtt ctg ggg acc ttc cac gga agt	1440
Ala Thr Tyr Asp Tyr Gly Thr Pro Val Leu Gly Thr Phe His Gly Ser	
465 470 475 480	
gac ctg ctg cag gtg ttc tat ggg atc aag cca aac tat gca gct agt	1488
Asp Leu Leu Gln Val Phe Tyr Gly Ile Lys Pro Asn Tyr Ala Ala Ser	
485 490 495	
tct agc cac acg tac tat ctg agc ttt gtg tat acg ctg gat ccg aac	1536
Ser Ser His Thr Tyr Tyr Leu Ser Phe Val Tyr Thr Leu Asp Pro Asn	
500 505 510	
tcc aac cgg ggg gag tac att gag tgg ccg cag tgg aag gaa tcg cgg	1584
Ser Asn Arg Gly Glu Tyr Ile Glu Trp Pro Gln Trp Lys Glu Ser Arg	
515 520 525	
cag ttg atg aat ttc gga gcg aac gac gcc agt ctc ctt acg gat gat	1632
Gln Leu Met Asn Phe Gly Ala Asn Asp Ala Ser Leu Leu Thr Asp Asp	
530 535 540	
ttc cgc aac ggg aca tat gag ttc atc ctg cag aat acc gcg gcg ttc	1680
Phe Arg Asn Gly Thr Tyr Glu Phe Ile Leu Gln Asn Thr Ala Ala Phe	
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cac atc tga	1689
His Ile	

<210> 12

<211> 562

<212> PRT

<213> Aspergillus niger

<400> 12

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His Pro Ser Ala Thr Val Ile Gly Lys Ser Gly Asn Val Glu Ser Phe	
35 40 45	
Asn Asn Ile Pro Phe Ala Gln Ala Pro Thr Gly Ser Leu Arg Leu Lys	
50 55 60	
Pro Pro Gln Pro Leu Glu Thr Ala Leu Gly Thr Val Gln Ala Thr Gly	
65 70 75 80	
Ala Ser Gln Ser Cys Pro Gln Met Tyr Phe Thr Thr Asp Glu Ser Glu	
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Phe Pro Thr Ser Val Ile Gly Leu Leu Ala Asp Leu Pro Leu Val Gln	

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Thr Met Val Ser Ser	Ser Ile Asp Lys Asn Met Pro Ile Val Phe Val				
	165		170		175
Ala Met Asn Tyr Arg	Val Gly Gly Phe Gly Phe Leu Pro Gly Lys Glu				
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Ile Leu Glu Asp Gly	Ser Ala Asn Leu Gly Leu Leu Asp Gln Arg Leu				
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Asp Lys Val Thr Ile	Trp Gly Glu Ser Ala Gly Ala Ile Ser Val Phe				
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Leu Phe Arg Gly Ala	Ile Met Asp Ser Gly Ser Val Val Pro Ala Asp				
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Pro Val Asp Gly Val	Lys Gly Gln Gln Val Tyr Asp Ala Val Val Glu				
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Leu Asp Tyr Thr Asp	Phe Leu Asn Ala Ala Asn Ser Val Pro Gly Ile				
305		310		315	320
Leu Ser Tyr His Ser	Val Ala Leu Ser Tyr Val Pro Arg Pro Asp Gly				
	325		330		335
Thr Ala Leu Ser Ala	Ser Pro Asp Val Leu Gly Lys Ala Gly Lys Tyr				
	340		345		350
Ala Arg Val Pro Phe	Ile Val Gly Asp Gln Glu Asp Glu Gly Thr Leu				
	355		360		365
Phe Ala Leu Phe Gln	Ser Asn Ile Thr Thr Ile Asp Glu Val Val Asp				
	370		375		380
Tyr Leu Ala Ser Tyr	Phe Phe Tyr Asp Ala Ser Arg Glu Gln Leu Glu				
385		390		395	400
Glu Leu Val Ala Leu	Tyr Pro Asp Thr Thr Thr Tyr Gly Ser Pro Phe				
	405		410		415
Arg Thr Gly Ala Ala	Asn Asn Trp Tyr Pro Gln Phe Lys Arg Leu Ala				
	420		425		430
Ala Ile Leu Gly Asp	Leu Val Phe Thr Ile Thr Arg Arg Ala Phe Leu				
	435		440		445
Ser Tyr Ala Glu Glu	Ile Ser Pro Asp Leu Pro Asn Trp Ser Tyr Leu				

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450 455 460
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 465 470 475 480
 Asp Leu Leu Gln Val Phe Tyr Gly Ile Lys Pro Asn Tyr Ala Ala Ser
 485 490 495
 Ser Ser His Thr Tyr Tyr Leu Ser Phe Val Tyr Thr Leu Asp Pro Asn
 500 505 510
 Ser Asn Arg Gly Glu Tyr Ile Glu Trp Pro Gln Trp Lys Glu Ser Arg
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 Gln Leu Met Asn Phe Gly Ala Asn Asp Ala Ser Leu Leu Thr Asp Asp
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 His Ile

<210> 13

<211> 2097

<212> DNA

<213> *Aspergillus niger*

<400> 13

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cgccttaggc	tacagcatca	acgacttctc	ctgcaatagc	accgaacacc	cgaatccagt	1260
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21078W0.ST25.txt

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gctacagacc caaggctatt gcacttacgc caaaacctac ggtgcatatg aaggcttccc 1380
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cgaggtgaaa gaaaagacgg gcgccgacaa gattgacctt gtcggtcact ccgaaggcgc 1500
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ttgtcctcta gacctgtcg gtcatatcgg tgaggcatac gatctgaacg tctggaatct 1920
ggtcaaaaac gccttggact ctacgccgaa gcgtgagttc gtctgctcgc tgggatctcc 1980
cggcaggtga gactatcatc ttctgaaaat ttgtatataa gcatttatat ttggataccc 2040
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<210> 14

<211> 834

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(834)

<400> 14

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1 5 10 15
tta ggc tac agc atc aac gac ttc tcc tgc aat agc acc gaa cac ccg 96
Leu Gly Tyr Ser Ile Asn Asp Phe Ser Cys Asn Ser Thr Glu His Pro
20 25 30
aat cca gtt gtg ctc cta cat ggg cta ggc gcc acc tac tac gaa gac 144
Asn Pro Val Val Leu Leu His Gly Leu Gly Ala Thr Tyr Tyr Glu Asp
35 40 45
ttg aat tac ctg caa ggt tgg cta cag acc caa ggc tat tgc act tac 192
Leu Asn Tyr Leu Gln Gly Trp Leu Gln Thr Gln Gly Tyr Cys Thr Tyr
50 55 60
gcc aaa acc tac ggt gca tat gaa ggc ttc ccc ttt gtc ggc ggc ctc 240
Ala Lys Thr Tyr Gly Ala Tyr Glu Gly Phe Pro Phe Val Gly Gly Leu
65 70 75 80
aag gcc atc gcc gaa tcg gcc acg gaa atc gcc gcg tac atc cgc gag 288
Lys Ala Ile Ala Glu Ser Ala Thr Glu Ile Ala Ala Tyr Ile Arg Glu
85 90 95
gtg aaa gaa aag acg ggc gcc gac aag att gac ctt gtc ggt cac tcc 336

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21078WO.ST25.txt

Val	Lys	Glu	Lys	Thr	Gly	Ala	Asp	Lys	Ile	Asp	Leu	Val	Gly	His	Ser		
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Glu	Gly	Ala	Phe	Gln	Thr	Leu	Tyr	Val	Pro	Lys	Phe	Glu	Asp	Gly	Ile		
		115					120					125					
tcg	gag	atg	ctg	gat	aag	ctg	gtg	gcc	att	gca	cct	ccc	acc	aga	ggc	432	
Ser	Glu	Met	Leu	Asp	Lys	Leu	Val	Ala	Ile	Ala	Pro	Pro	Thr	Arg	Gly		
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acc	aac	ttg	gcg	ggg	atc	tat	gac	atc	gca	tat	gtt	ctg	gga	aat	cta	480	
Thr	Asn	Leu	Ala	Gly	Ile	Tyr	Asp	Ile	Ala	Tyr	Val	Leu	Gly	Asn	Leu		
145					150				155					160			
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Ser	Arg	Asp	Leu	Ile	Gly	Asp	Val	Leu	Asp	Thr	Val	Gly	Cys	Ala	Ala		
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Cys	Asp	Asp	Leu	Gly	Pro	Asp	Gly	Ala	Ala	Ile	Asp	Arg	Leu	Asn	Asp		
			180				185				190						
ggc	gag	cct	atc	gtg	cag	ccg	gga	aat	aat	cta	acg	gtg	att	gca	tcg	624	
Gly	Glu	Pro	Ile	Val	Gln	Pro	Gly	Asn	Asn	Leu	Thr	Val	Ile	Ala	Ser		
		195				200					205						
cgg	tcc	gac	gaa	ttg	gtc	acc	cca	acc	acc	acc	tcc	ttc	gtg	cat	gaa	672	
Arg	Ser	Asp	Glu	Leu	Val	Thr	Pro	Thr	Thr	Thr	Ser	Phe	Val	His	Glu		
		210				215					220						
gat	ggg	gtg	acc	aat	gaa	tgg	gtg	caa	gac	act	tgt	cct	cta	gac	cct	720	
Asp	Gly	Val	Thr	Asn	Glu	Trp	Val	Gln	Asp	Thr	Cys	Pro	Leu	Asp	Pro		
225					230				235					240			
gtc	ggt	cat	atc	ggt	gag	gca	tac	gat	ctg	aac	gtc	tgg	aat	ttg	gtc	768	
Val	Gly	His	Ile	Gly	Glu	Ala	Tyr	Asp	Leu	Asn	Val	Trp	Asn	Leu	Val		
			245					250			255						
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Lys	Asn	Ala	Leu	Asp	Ser	Thr	Pro	Lys	Arg	Glu	Phe	Val	Cys	Ser	Leu		
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gga	tct	ccc	ggc	agg	tga											834	
Gly	Ser	Pro	Gly	Arg													
		275															

<210> 15

<211> 277

<212> PRT

<213> Aspergillus niger

<400> 15

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21078W0.ST25.txt

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           35           40           45
Leu Asn Tyr Leu Gln Gly Trp Leu Gln Thr Gln Gly Tyr Cys Thr Tyr
           50           55           60
Ala Lys Thr Tyr Gly Ala Tyr Glu Gly Phe Pro Phe Val Gly Gly Leu
65           70           75           80
Lys Ala Ile Ala Glu Ser Ala Thr Glu Ile Ala Ala Tyr Ile Arg Glu
           85           90           95
Val Lys Glu Lys Thr Gly Ala Asp Lys Ile Asp Leu Val Gly His Ser
           100          105          110
Glu Gly Ala Phe Gln Thr Leu Tyr Val Pro Lys Phe Glu Asp Gly Ile
           115          120          125
Ser Glu Met Leu Asp Lys Leu Val Ala Ile Ala Pro Pro Thr Arg Gly
           130          135          140
Thr Asn Leu Ala Gly Ile Tyr Asp Ile Ala Tyr Val Leu Gly Asn Leu
145          150          155          160
Ser Arg Asp Leu Ile Gly Asp Val Leu Asp Thr Val Gly Cys Ala Ala
           165          170          175
Cys Asp Asp Leu Gly Pro Asp Gly Ala Ala Ile Asp Arg Leu Asn Asp
           180          185          190
Gly Glu Pro Ile Val Gln Pro Gly Asn Asn Leu Thr Val Ile Ala Ser
           195          200          205
Arg Ser Asp Glu Leu Val Thr Pro Thr Thr Thr Ser Phe Val His Glu
           210          215          220
Asp Gly Val Thr Asn Glu Trp Val Gln Asp Thr Cys Pro Leu Asp Pro
225          230          235          240
Val Gly His Ile Gly Glu Ala Tyr Asp Leu Asn Val Trp Asn Leu Val
           245          250          255
Lys Asn Ala Leu Asp Ser Thr Pro Lys Arg Glu Phe Val Cys Ser Leu
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Gly Ser Pro Gly Arg
           275

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<210> 16

<211> 1881

<212> DNA

<213> Aspergillus niger

<400> 16

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21078WO.ST25.txt

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gaaattatta	ataccgagct	ggtctgccc	tttttcccaa	accttccctc	tttccatccc	360
tctcgctcg	cacccctttt	atcctccctc	ccgccatgta	tatccctctg	gtgctgcttc	420
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cccaccagat	cgcctacgat	tcgttcgacg	tcaatgccag	tcccagctac	gcatgtaca	780
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gcttcatgaa	catggtacga	aagattagat	tatgtatata	gtgtggaagt	ggtaatgatg	1800
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<210> 17

<211> 1257

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(1257)

<400> 17

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21078W0.ST25.txt

Met Tyr Ile Pro Ser Val Leu Leu Leu Ala Ala Ser Leu Phe His Gly	
1 5 10 15	
gca acg gcg ctg ccc acg ccc ggc tcc acg ccc atc ccg ccc agc cag	96
Ala Thr Ala Leu Pro Thr Pro Gly Ser Thr Pro Ile Pro Pro Ser Gln	
20 25 30	
gat ccc tgg tac agt gcg ccc gag ggc ttc gag gag gct gat ccc ggt	144
Asp Pro Trp Tyr Ser Ala Pro Glu Gly Phe Glu Glu Ala Asp Pro Gly	
35 40 45	
gcc atc ctg cgc gtg cgg ccc gcg ccc ggc aac ttg acc gtg gta gtg	192
Ala Ile Leu Arg Val Arg Pro Ala Pro Gly Asn Leu Thr Val Val Val	
50 55 60	
ggc aat gcg tcg gcg gcc tac aac atc ctc tac cgc act aca gac agt	240
Gly Asn Ala Ser Ala Ala Tyr Asn Ile Leu Tyr Arg Thr Thr Asp Ser	
65 70 75 80	
cag tac aag ccc tcc tgg gct gtg acc acc ctg ctg gtg ccc ccc gtg	288
Gln Tyr Lys Pro Ser Trp Ala Val Thr Thr Leu Leu Val Pro Pro Val	
85 90 95	
gcc gcc tcc gcc gcc gtc aac cag agt gtc ctg ctc tcc cac cag atc	336
Ala Ala Ser Ala Ala Val Asn Gln Ser Val Leu Leu Ser His Gln Ile	
100 105 110	
gcc tac gat tcg ttc gac gtc aat gcc agt ccc agc tac gcc atg tac	384
Ala Tyr Asp Ser Phe Asp Val Asn Ala Ser Pro Ser Tyr Ala Met Tyr	
115 120 125	
acc agc ccg ccc tcc gat att atc ctc gcc ctg cag cgc ggc tgg ttc	432
Thr Ser Pro Pro Ser Asp Ile Ile Leu Ala Leu Gln Arg Gly Trp Phe	
130 135 140	
gtt aac gtc ccc gat tac gag ggc ccc aat gcc tct ttc acc gcc ggt	480
Val Asn Val Pro Asp Tyr Glu Gly Pro Asn Ala Ser Phe Thr Ala Gly	
145 150 155 160	
gtg cag tcc ggc cat gcc acc ctc gac tcg gtc cgc agc gtg ctc gcc	528
Val Gln Ser Gly His Ala Thr Leu Asp Ser Val Arg Ser Val Leu Ala	
165 170 175	
tcc gga ttc ggc ctg aac gag gac gcc cag tac gct ctg tgg ggt tac	576
Ser Gly Phe Gly Leu Asn Glu Asp Ala Gln Tyr Ala Leu Trp Gly Tyr	
180 185 190	
tct ggc ggt gcc ttg gcc agc gaa tgg gct gct gaa ctg cag atg caa	624
Ser Gly Gly Ala Leu Ala Ser Glu Trp Ala Ala Glu Leu Gln Met Gln	
195 200 205	
tac gct ccc gag ttg aac att gcc ggt ctg gcc gtg ggt ggt ctc act	672
Tyr Ala Pro Glu Leu Asn Ile Ala Gly Leu Ala Val Gly Gly Leu Thr	
210 215 220	
ccc aat gtt acc agc gtc atg gac acg gtg acc tcg acc atc agt gcg	720
Pro Asn Val Thr Ser Val Met Asp Thr Val Thr Ser Thr Ile Ser Ala	
225 230 235 240	

21078W0.ST25.txt

gga ctc atc ccc gcc gcc gcc ctg ggt ctg tcg agc cag cac ccc gag	768
Gly Leu Ile Pro Ala Ala Ala Leu Gly Leu Ser Ser Gln His Pro Glu	
245 250 255	
acc tac gag ttc atc ctc agc cag ctc aag acg acg gga ccc tac aac	816
Thr Tyr Glu Phe Ile Leu Ser Gln Leu Lys Thr Thr Gly Pro Tyr Asn	
260 265 270	
cgc aca gga ttc cta gcc gcc aag gac ctg acc ctg tcc gag gcg gag	864
Arg Thr Gly Phe Leu Ala Ala Lys Asp Leu Thr Leu Ser Glu Ala Glu	
275 280 285	
gtc ttc tac gcc ttc cag aac atc ttc gat tac ttt gtc aac gga tcg	912
Val Phe Tyr Ala Phe Gln Asn Ile Phe Asp Tyr Phe Val Asn Gly Ser	
290 295 300	
gcc acg ttc cag gcg gag gtg gtg cag aag gcg ctg aac cag gac gga	960
Ala Thr Phe Gln Ala Glu Val Val Gln Lys Ala Leu Asn Gln Asp Gly	
305 310 315 320	
tac atg ggc tac cat ggg ttc ccg cag atg ccg gtg ctc gcg tac aag	1008
Tyr Met Gly Tyr His Gly Phe Pro Gln Met Pro Val Leu Ala Tyr Lys	
325 330 335	
gct att cac gat gag atc agt ccc atc cag gat acg gat cgc gtg atc	1056
Ala Ile His Asp Glu Ile Ser Pro Ile Gln Asp Thr Asp Arg Val Ile	
340 345 350	
aag cgc tac tgt ggt ctg gga ttg aac atc ttg tat gag cgg aac acc	1104
Lys Arg Tyr Cys Gly Leu Gly Leu Asn Ile Leu Tyr Glu Arg Asn Thr	
355 360 365	
atc ggt ggc cac tcg gca gag cag gtg aat ggc aac gcc agg gcg tgg	1152
Ile Gly Gly His Ser Ala Glu Gln Val Asn Gly Asn Ala Arg Ala Trp	
370 375 380	
aac tgg ttg acg agc att ttc gac gga acg tat gcg cag cag tac aag	1200
Asn Trp Leu Thr Ser Ile Phe Asp Gly Thr Tyr Ala Gln Gln Tyr Lys	
385 390 395 400	
acc gag ggg tgc acg atc cgc aat gtc act ctg aac acg act tcc tcc	1248
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Val Tyr	

<210> 18

<211> 418

<212> PRT

<213> Aspergillus niger

<400> 18

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21078W0.ST25.txt

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Ala Ile Leu Arg Val Arg Pro Ala Pro Gly Asn Leu Thr Val Val Val
          50           55           60
Gly Asn Ala Ser Ala Ala Tyr Asn Ile Leu Tyr Arg Thr Thr Asp Ser
65           70           75           80
Gln Tyr Lys Pro Ser Trp Ala Val Thr Thr Leu Leu Val Pro Pro Val
          85           90           95
Ala Ala Ser Ala Ala Val Asn Gln Ser Val Leu Leu Ser His Gln Ile
          100          105          110
Ala Tyr Asp Ser Phe Asp Val Asn Ala Ser Pro Ser Tyr Ala Met Tyr
          115          120          125
Thr Ser Pro Pro Ser Asp Ile Ile Leu Ala Leu Gln Arg Gly Trp Phe
          130          135          140
Val Asn Val Pro Asp Tyr Glu Gly Pro Asn Ala Ser Phe Thr Ala Gly
145          150          155          160
Val Gln Ser Gly His Ala Thr Leu Asp Ser Val Arg Ser Val Leu Ala
          165          170          175
Ser Gly Phe Gly Leu Asn Glu Asp Ala Gln Tyr Ala Leu Trp Gly Tyr
          180          185          190
Ser Gly Gly Ala Leu Ala Ser Glu Trp Ala Ala Glu Leu Gln Met Gln
          195          200          205
Tyr Ala Pro Glu Leu Asn Ile Ala Gly Leu Ala Val Gly Gly Leu Thr
          210          215          220
Pro Asn Val Thr Ser Val Met Asp Thr Val Thr Ser Thr Ile Ser Ala
225          230          235          240
Gly Leu Ile Pro Ala Ala Ala Leu Gly Leu Ser Ser Gln His Pro Glu
          245          250          255
Thr Tyr Glu Phe Ile Leu Ser Gln Leu Lys Thr Thr Gly Pro Tyr Asn
          260          265          270
Arg Thr Gly Phe Leu Ala Ala Lys Asp Leu Thr Leu Ser Glu Ala Glu
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Val Phe Tyr Ala Phe Gln Asn Ile Phe Asp Tyr Phe Val Asn Gly Ser
          290          295          300
Ala Thr Phe Gln Ala Glu Val Val Gln Lys Ala Leu Asn Gln Asp Gly
305          310          315          320
Tyr Met Gly Tyr His Gly Phe Pro Gln Met Pro Val Leu Ala Tyr Lys
          325          330          335
Ala Ile His Asp Glu Ile Ser Pro Ile Gln Asp Thr Asp Arg Val Ile
          340          345          350
Lys Arg Tyr Cys Gly Leu Gly Leu Asn Ile Leu Tyr Glu Arg Asn Thr

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21078WO.ST25.txt

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 370 375 380
 Asn Trp Leu Thr Ser Ile Phe Asp Gly Thr Tyr Ala Gln Gln Tyr Lys
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 Thr Glu Gly Cys Thr Ile Arg Asn Val Thr Leu Asn Thr Thr Ser Ser
 405 410 415
 Val Tyr

<210> 19

<211> 2809

<212> DNA

<213> Aspergillus niger

<400> 19

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tcctcttccc	ctagtcatgc	ggcttgggt	ctttgaagca	ttgcttcggc	gcattatggg	1200
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aaagaagaga	aaattgctgc	gtcgggtgct	ctggcgctcg	acttcacgga	tatatgcgcg	1620
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21078WO.ST25.txt

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<211> 1413

<212> DNA

<213> *Aspergillus niger*

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<222> (1)..(1413)

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Ala	Leu	Phe	Gly	Ser	Leu	Ile	Leu	Val	Leu	Leu	Glu	Trp	Val	Ile	His	
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att	atc	aca	ttc	tgt	ctg	cct	gaa	cct	ggt	att	aag	ttc	tgt	tac	gat	144
Ile	Ile	Thr	Phe	Cys	Leu	Pro	Glu	Pro	Val	Ile	Lys	Phe	Cys	Tyr	Asp	
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cga	tcc	aag	act	atc	ttc	aac	gcc	ttc	att	cct	ccc	gat	gac	ccg	gct	192
Arg	Ser	Lys	Thr	Ile	Phe	Asn	Ala	Phe	Ile	Pro	Pro	Asp	Asp	Pro	Ala	
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Trp	Asp	Phe	Ser	Ile	Asp	Gln	Phe	Ser	Phe	His	Asp	Ile	Pro	Asp	Ser		
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Ala	Ser	Pro	Asn	Phe	Leu	Phe	Leu	Leu	Phe	Gly	Arg	Arg	Ser	Ile	Leu		
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 Asp Phe Thr Asp Ile Cys Ala Leu Phe Gly Tyr Glu Ala Glu Glu His
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 Tyr Arg Lys Gly Glu Glu Gly Arg Lys Ile Asn Gln Gly Glu Gly Ser
 115 120 125
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 Leu Val Glu Arg Gly Tyr Asp Val Trp Leu Gly Asn Asn Arg Gly Asn
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 Lys Tyr Ser Lys Lys Ser Val Lys His Ser Pro Leu Ser Asn Glu Phe
 180 185 190
 Trp Asp Phe Ser Ile Asp Gln Phe Ser Phe His Asp Ile Pro Asp Ser
 195 200 205
 Ile Lys Tyr Ile Leu Glu Val Thr Gly Gln Pro Ser Leu Ser Tyr Val
 210 215 220
 Gly Phe Ser Gln Gly Thr Ala Gln Ala Phe Ala Thr Leu Ser Ile His
 225 230 235 240
 Pro Leu Leu Asn Gln Lys Ile Asp Val Phe Val Ala Leu Ala Pro Ala
 245 250 255
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 260 265 270
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 Trp Ile Ile Asp Thr Ser Leu Arg Gly Leu Phe Asn Trp Arg Cys Lys
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 325 330 335
 Phe Thr Ser Thr Lys Ser Val Val His Trp Phe Gln Ile Ile Arg His
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 Val Ala Ser Glu Arg Phe Tyr Lys Pro Val Lys Tyr Pro Thr Lys Asn

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370 375 380
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<210> 22

<211> 3328

<212> DNA

<213> *Aspergillus niger*

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<210> 23

<211> 1779

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

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Leu Leu Phe Ala Gln Gln Leu Ala Ser His Pro Thr Glu Gln Ile Gln	
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gcc att ctg gct ccg tgg gtc ccg gcc gca cta caa gat gtc gtg ctc	144
Ala Ile Leu Ala Pro Trp Val Pro Ala Ala Leu Gln Asp Val Val Leu	
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Tyr Asn Arg Pro Arg Val Ile Ile Pro Gln Gly Thr Val Val Gly Thr	
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Thr Leu Thr Asp Thr Leu Lys Ser Pro Val Asp Ala Phe Arg Gly Ile	
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Pro Tyr Ala Leu Pro Pro Ile Gly Asp Arg Arg Phe Arg Arg Ala Glu	
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Ala Val His Ala Thr Asp Glu Ile Ile Asp Ala Ser Glu Phe Gly Pro	
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Arg Cys Pro Gly Lys Gln Leu Leu Asn Pro Asn Asp Ile Gly Gly Asp	
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Gln	Phe	Thr	Asp	Phe	Leu	Thr	Glu	Thr	Gly	Cys	Thr	Asn	Leu	Pro	Asp	
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Ala	Phe	Gln	Pro	Val	Ile	Asp	His	Glu	Ile	Ile	His	Arg	Arg	Pro	Ile	
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[illegible]

<213> *Aspergillus niger*

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			20					25					30		
Ala	Ile	Leu	Ala	Pro	Trp	Val	Pro	Ala	Ala	Leu	Gln	Asp	Val	Val	Leu
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Tyr	Asn	Arg	Pro	Arg	Val	Ile	Ile	Pro	Gln	Gly	Thr	Val	Val	Gly	Thr
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Pro	Tyr	Ala	Leu	Pro	Pro	Ile	Gly	Asp	Arg	Arg	Phe	Arg	Arg	Ala	Glu

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	85		90		95
Ala Val His	Ala Thr Asp Glu Ile	Ile Asp Ala Ser	Glu Phe Gly Pro		
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Arg Cys Pro	Gly Lys Gln Leu Leu	Asn Pro Asn Asp	Ile Gly Gly Asp		
	115	120	125		
Glu Asp Cys	Leu Thr Val Asn Val	Phe Arg Pro His	Gly Ala Gln Gly		
	130	135	140		
Lys Leu Pro	Val Ala Val Tyr Val	His Gly Gly Ala	Tyr Asn Arg Gly		
145	150	155	160		
Thr Ala Lys	Tyr Pro Ala Ser Gly	His Asn Thr Ala	Ser Met Val Gly		
	165	170	175		
Trp Ser Asp	Glu Pro Phe Val Ala	Val Ser Phe Asn	Tyr Arg Ile Gly		
	180	185	190		
Ala Leu Gly	Phe Leu Pro Ser Thr	Leu Thr Ala Lys	Glu Gly Ile Leu		
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Asn Leu Gly	Leu His Asp Gln Ile	Leu Leu Leu Gln	Trp Val Gln Glu		
	210	215	220		
Asn Ile Ala	His Phe Asn Gly Asp	Pro Thr Gln Val	Thr Leu Ile Gly		
225	230	235	240		
Leu Ser Ala	Gly Ala His Ser Ile	Ala His His Ile	Met Asn Tyr Asn		
	245	250	255		
Pro Pro Asn	Thr Pro Leu Phe His	Arg Ala Ile Ile	Glu Ser Gly Ala		
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Ala Thr Ser	Arg Ala Val His Pro	Tyr Asn Ala Ser	Leu His Glu Ser		
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Gln Phe Thr	Asp Phe Leu Thr Glu	Thr Gly Cys Thr	Asn Leu Pro Asp		
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Thr Ala Ile	Leu Pro Cys Leu Arg	Ala Leu Pro Ser	Ser Ala Ile Thr		
305	310	315	320		
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	325	330	335		
Ala Phe Gln	Pro Val Ile Asp His	Glu Ile Ile His	Arg Arg Pro Ile		
	340	345	350		
Asp Ala Trp	Arg Ser Gly Lys Trp	Asn Arg Met Pro	Ile Leu Thr Gly		
	355	360	365		
Phe Asn Ser	Asn Glu Gly Thr Tyr	Tyr Val Pro Arg	Asn Leu Ser Leu		
	370	375	380		
Ser Glu Asp	Phe Thr Ser Phe Phe	Arg Thr Leu Leu	Pro Ala Tyr Pro		
385	390	395	400		
Glu Ser Asp	Ile Gln Thr Ile Asp	Glu Ile Tyr Pro	Asp Pro Asn Val		
	405	410	415		
Tyr Ala Thr	Ala Ser Pro Tyr Leu	Glu Thr Arg Pro	Ile Pro Ser Leu		
	420	425	430		
Gly Arg Gln	Phe Lys Arg Leu Glu	Ala Ala Tyr Gly	His Tyr Ala Tyr		

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435 440 445
 Ala Cys Pro Val Arg Gln Thr Ala Gly Phe Val Ala Asn Asp Asp Gly
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 465 470 475 480
 Ile Gly Gly Ala Asn His Gly Asp Gln Met Glu Tyr Glu Thr Phe Asn
 485 490 495
 Pro Ala Val Arg Asp Ile Ser Glu Ala Gln Arg Glu Val Ala Gly Leu
 500 505 510
 Phe His Ala Tyr Val Thr Ser Phe Val Val His Gly Asp Pro Asn Val
 515 520 525
 Leu Gly Gly Arg Tyr Glu Gly Arg Glu Val Trp Glu Arg Tyr Ser Gly
 530 535 540
 Glu Gly Gly Glu Val Met Val Phe Gly Glu Gly Asn Asp Glu Arg Ala
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 Gly Gly Asp Gly Val Gly Val Ala Ala Arg Leu Lys Arg Asp Glu Trp
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 Gly Val Lys Glu Cys Gly Phe Trp Ser Gly Arg Ser Gly Ile Ser Glu
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<210> 25

<211> 3932

<212> DNA

<213> *Aspergillus niger*

<400> 25

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aagaattgag	gttacatcga	ccgatagggc	tcttaatcca	accctcttca	cggggaaaac	360
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tatggcatgg	cgtgtgggaa	ccgatcaatt	tgtataatat	cttaggccca	cctcttcccc	1020
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caatctcaac atgtgggctc ttacgctgtc atcatattag ttaggggtcca agagaatcac	3900
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<210> 26

<211> 1518

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(1518)

<400> 26

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aca ctc gct tct aca cag aat gcc gat aca ccg aca tcc gct cct act	96
Thr Leu Ala Ser Thr Gln Asn Ala Asp Thr Pro Thr Ser Ala Pro Thr	
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Val Gln Val Arg Asn Gly Thr Tyr Glu Gly Leu Tyr Asn Pro Thr Tyr	
35 40 45	
aat cag gac ttg ttc ctc ggc ata ccg tat gcg cag cct ccg gtt ggt	192
Asn Gln Asp Leu Phe Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly	
50 55 60	
gag cta cga ttc cgt cca cca caa ccg ctc aac acg acg tgg act ggc	240
Glu Leu Arg Phe Arg Pro Pro Gln Pro Leu Asn Thr Thr Trp Thr Gly	
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act cga aat gca aca gcc tat tac aat gaa tgt atc ggt tat ggt agc	288
Thr Arg Asn Ala Thr Ala Tyr Tyr Asn Glu Cys Ile Gly Tyr Gly Ser	
85 90 95	
gac gac tgg tat tgg acc gac gta gtc tcc gaa gat tgt ctc gct ctc	336
Asp Asp Trp Tyr Trp Thr Asp Val Val Ser Glu Asp Cys Leu Ala Leu	
100 105 110	
agt gtg att cga cct cac ggc atc gac tca agc gcg aag ctg ccc gtc	384
Ser Val Ile Arg Pro His Gly Ile Asp Ser Ser Ala Lys Leu Pro Val	
115 120 125	
gtc ttc tgg atg cat ggt gga gaa ttc gca gaa gga ggc act cgc gac	432
Val Phe Trp Met His Gly Gly Glu Phe Ala Glu Gly Gly Thr Arg Asp	
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Ser	Pro	Ile	Ile	Gly	Val	Thr	Val	Asn	Tyr	Arg	Leu	Ser	Gly	Trp	Gly	
				165				170						175		
ttc	ctc	tat	agc	cag	gaa	gtc	gcc	gac	gaa	ggc	tcc	gcc	aac	tta	gga	576
Phe	Leu	Tyr	Ser	Gln	Glu	Val	Ala	Asp	Glu	Gly	Ser	Ala	Asn	Leu	Gly	
			180					185					190			
ctc	cgc	gac	caa	cgg	cac	gct	ctg	tac	tgg	ctc	caa	gag	aat	atc	gct	624
Leu	Arg	Asp	Gln	Arg	His	Ala	Leu	Tyr	Trp	Leu	Gln	Glu	Asn	Ile	Ala	
		195					200					205				
tcc	ttc	ggc	ggc	gac	ccg	tcg	cgg	ctc	acc	atc	tgg	ggc	caa	agt	gcc	672
Ser	Phe	Gly	Gly	Asp	Pro	Ser	Arg	Leu	Thr	Ile	Trp	Gly	Gln	Ser	Ala	
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ggt	gcc	aac	agc	gtc	ggt	ctc	cat	tta	gtg	gca	tac	gac	ggc	cag	aat	720
Gly	Ala	Asn	Ser	Val	Gly	Leu	His	Leu	Val	Ala	Tyr	Asp	Gly	Gln	Asn	
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gat	ggc	atc	ttc	cgt	gcc	ggg	atc	gcc	gag	agc	ggc	tcc	gta	ccc	tcc	768
Asp	Gly	Ile	Phe	Arg	Ala	Gly	Ile	Ala	Glu	Ser	Gly	Ser	Val	Pro	Ser	
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ctc	gca	gca	tac	atg	agc	gcc	gaa	gat	gca	caa	cca	tac	tat	gat	gcc	816
Leu	Ala	Ala	Tyr	Met	Ser	Ala	Glu	Asp	Ala	Gln	Pro	Tyr	Tyr	Asp	Ala	
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gtc	gtc	aac	gca	acc	aac	tgc	acc	ggc	tct	tcc	aac	acc	ctt	act	tgt	864
Val	Val	Asn	Ala	Thr	Asn	Cys	Thr	Gly	Ser	Ser	Asn	Thr	Leu	Thr	Cys	
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Leu	Arg	Glu	Val	Pro	Thr	Asp	Val	Leu	Ser	Ser	Ile	Phe	Asn	Ser	Ser	
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ctc	gtc	gct	ggg	gca	gga	tat	cat	ccc	gtc	att	gac	ggc	gat	ttc	ctc	960
Leu	Val	Ala	Gly	Ala	Gly	Tyr	His	Pro	Val	Ile	Asp	Gly	Asp	Phe	Leu	
305				310					315						320	
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Arg	Ala	Ser	Gly	Ile	Val	Asn	Leu	Gln	Thr	Gly	Gln	Phe	Ala	Lys	Thr	
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Pro	Leu	Leu	Ile	Gly	Thr	Asn	Phe	Asp	Glu	Gly	Thr	Lys	Tyr	Ala	Pro	
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Ser Tyr Gly Tyr Gln Trp Lys Arg Val Ala Ala Phe Leu Gly Asp Leu
          405          410          415
ctc atg cac gcg cct cgc cgc gtg aca acc cag tgg ctg gca cac tgg      1296
Leu Met His Ala Pro Arg Arg Val Thr Thr Gln Trp Leu Ala His Trp
          420          425          430
aat gta cct gcc tac gtg tat cac tgg aac gtg atg aca cta ggg cca      1344
Asn Val Pro Ala Tyr Val Tyr His Trp Asn Val Met Thr Leu Gly Pro
          435          440          445
tta gat gga gcc gcg cat ggc tat gaa gtc ccc ttc agt ttc cat aat      1392
Leu Asp Gly Ala Ala His Gly Tyr Glu Val Pro Phe Ser Phe His Asn
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tat gat ggt ttg ggc gat gaa cgg gga aac gac agc gtg acc tgg cca      1440
Tyr Asp Gly Leu Gly Asp Glu Arg Gly Asn Asp Ser Val Thr Trp Pro
465          470          475          480
caa cta tcg act atg atg tca cgg atg tgg gtg agc ttt att aat cat      1488
Gln Leu Ser Thr Met Met Ser Arg Met Trp Val Ser Phe Ile Asn His
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ttg gat ccg aat tat agt aat agt gag tga      1518
Leu Asp Pro Asn Tyr Ser Asn Ser Glu
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<210> 27

<211> 505

<212> PRT

<213> *Aspergillus niger*

<400> 27

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Val Gln Val Arg Asn Gly Thr Tyr Glu Gly Leu Tyr Asn Pro Thr Tyr
          35          40          45
Asn Gln Asp Leu Phe Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly
          50          55          60
Glu Leu Arg Phe Arg Pro Pro Gln Pro Leu Asn Thr Thr Trp Thr Gly
65          70          75          80
Thr Arg Asn Ala Thr Ala Tyr Tyr Asn Glu Cys Ile Gly Tyr Gly Ser
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 Ser Arg Tyr Asn Leu Ser Tyr Ile Val Gln Gln Ser Gln Glu Met Gln
 145 150 155 160
 Ser Pro Ile Ile Gly Val Thr Val Asn Tyr Arg Leu Ser Gly Trp Gly
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 275 280 285
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 325 330 335
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 370 375 380
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 Ser Tyr Gly Tyr Gln Trp Lys Arg Val Ala Ala Phe Leu Gly Asp Leu
 405 410 415
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 Asn Val Pro Ala Tyr Val Tyr His Trp Asn Val Met Thr Leu Gly Pro
 435 440 445

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Leu Asp Gly Ala Ala His Gly Tyr Glu Val Pro Phe Ser Phe His Asn
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 Tyr Asp Gly Leu Gly Asp Glu Arg Gly Asn Asp Ser Val Thr Trp Pro
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<210> 28

<211> 3091

<212> DNA

<213> *Aspergillus niger*

<400> 28

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taatttcagg	gtcctgtcga	gcccagtcga	ggttccttag	tttcgatcct	tcagttggcc	360
cgtcatgtcc	attgaccagg	aatggagcaa	gccccgatga	ggatcggcca	gcggagacaa	420
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<210> 32

<211> 1695

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

21078W0.ST25.txt

<222> (1)..(1695)

<400> 32

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agc ctg gca acc tgc acc aac cca gta gcc cag aca aag aac gga agt	96
Ser Leu Ala Thr Cys Thr Asn Pro Val Ala Gln Thr Lys Asn Gly Ser	
20 25 30	
tat tat ggt gtc tac atg cct cag tat aat gag gat tat ttt ctt gga	144
Tyr Tyr Gly Val Tyr Met Pro Gln Tyr Asn Glu Asp Tyr Phe Leu Gly	
35 40 45	
att cca ttt gct aag ccc ccg ttg gca cac ttg cgt tgg gcc aac ccc	192
Ile Pro Phe Ala Lys Pro Pro Leu Ala His Leu Arg Trp Ala Asn Pro	
50 55 60	
gag agt ctt aat gag tct tgg tcg gga ttg cgc cct gct acc ggc tat	240
Glu Ser Leu Asn Glu Ser Trp Ser Gly Leu Arg Pro Ala Thr Gly Tyr	
65 70 75 80	
gcg atg gaa tgt ata ggt tac ggc agt gat caa aaa ggt tat ctg cag	288
Ala Met Glu Cys Ile Gly Tyr Gly Ser Asp Gln Lys Gly Tyr Leu Gln	
85 90 95	
agc gag gac tgt ctc tac cta aac gtg gtc cgt ccc gct gaa tac gac	336
Ser Glu Asp Cys Leu Tyr Leu Asn Val Val Arg Pro Ala Glu Tyr Asp	
100 105 110	
aat gcc agt ctt cca gtc ctt gta tgg att cat ggc ggt ggc ttc gca	384
Asn Ala Ser Leu Pro Val Leu Val Trp Ile His Gly Gly Gly Phe Ala	
115 120 125	
caa ggc ggc act ccc gac ctt cga tac aat ctt aca ttt att gtt gaa	432
Gln Gly Gly Thr Pro Asp Leu Arg Tyr Asn Leu Thr Phe Ile Val Glu	
130 135 140	
cac tcg gtc aat atc ggc cag cca att atc gca gtg agc gtt gcc tat	480
His Ser Val Asn Ile Gly Gln Pro Ile Ile Ala Val Ser Val Ala Tyr	
145 150 155 160	
cgt ctc ggt cct tgg ggt ttc ttc aat ggg gtc gag ctc gcc aat gag	528
Arg Leu Gly Pro Trp Gly Phe Phe Asn Gly Val Glu Leu Ala Asn Glu	
165 170 175	
gga tcg tta aat ctc ggg ctg aag gac cag cgc ttg gcc ctg cat tgg	576
Gly Ser Leu Asn Leu Gly Leu Lys Asp Gln Arg Leu Ala Leu His Trp	
180 185 190	
gtg aaa gag aac att gca ggt ttc ggt ggc gac cct agt aaa gtc gtg	624
Val Lys Glu Asn Ile Ala Gly Phe Gly Gly Asp Pro Ser Lys Val Val	
195 200 205	
att tac gga caa agt gcc ggc tcc gaa agc gtg gga tac caa atc cgc	672
Ile Tyr Gly Gln Ser Ala Gly Ser Glu Ser Val Gly Tyr Gln Ile Arg	

21078WO.ST25.txt

210	215	220	
gcg tac aac ggc cga gat gac ggg ctc ttc cgc gga ggc atg atg gag			720
Ala Tyr Asn Gly Arg Asp Asp Gly Leu Phe Arg Gly Gly Met Met Glu			
225	230	235	240
tcc ggc gcg gtg tta cct ggc agt gcc ttg aac ctc acc tgg aca tat			768
Ser Gly Ala Val Leu Pro Gly Ser Ala Leu Asn Leu Thr Trp Thr Tyr			
245	250	255	
gag cct tgg ttc cag caa ata gca gac gag gca gga tgt tcc cag acc			816
Glu Pro Trp Phe Gln Gln Ile Ala Asp Glu Ala Gly Cys Ser Gln Thr			
260	265	270	
acc cgc aaa ctg gac tgt cta cgc cgc acg ccc ttc aca gtc cta aac			864
Thr Arg Lys Leu Asp Cys Leu Arg Arg Thr Pro Phe Thr Val Leu Asn			
275	280	285	
aac att ctg aac acc acc gcc aac gac acg acg cct tac aac tgg agg			912
Asn Ile Leu Asn Thr Thr Ala Asn Asp Thr Thr Pro Tyr Asn Trp Arg			
290	295	300	
ccc aca gtg gac ggt gac ttc gta gcg cga tat ccc agc gag caa ctc			960
Pro Thr Val Asp Gly Asp Phe Val Ala Arg Tyr Pro Ser Glu Gln Leu			
305	310	315	320
gac aca gga gac ttc gtc aaa gta cca atc ata atc ggc tac acc acg			1008
Asp Thr Gly Asp Phe Val Lys Val Pro Ile Ile Ile Gly Tyr Thr Thr			
325	330	335	
gac gaa gga aca aca gag tgc cca gaa cca gtg aac acc acc gcc gaa			1056
Asp Glu Gly Thr Thr Glu Cys Pro Glu Pro Val Asn Thr Thr Ala Glu			
340	345	350	
tta aaa gaa tac ctc agc tca aca aca acc tac ggc tgg gcc ctc gac			1104
Leu Lys Glu Tyr Leu Ser Ser Thr Thr Thr Tyr Gly Trp Ala Leu Asp			
355	360	365	
tca cag gta gta tcc tcg ctc ctg gac ctc tac ccc aac acc acc tcc			1152
Ser Gln Val Val Ser Ser Leu Leu Asp Leu Tyr Pro Asn Thr Thr Ser			
370	375	380	
ttc ggc atc cca tca tcc gaa gaa ctc ggc ggc aac gtc acc ttc cca			1200
Phe Gly Ile Pro Ser Ser Glu Glu Leu Gly Gly Asn Val Thr Phe Pro			
385	390	395	400
cag ccc tac ggc gcc gca ttc cgc cag acg gca gca tac tac ggc gac			1248
Gln Pro Tyr Gly Ala Ala Phe Arg Gln Thr Ala Ala Tyr Tyr Gly Asp			
405	410	415	
gcc cag ttc ata gcc gcg acg cgc tac acc tgt gag cta tgg gcg gca			1296
Ala Gln Phe Ile Ala Ala Thr Arg Tyr Thr Cys Glu Leu Trp Ala Ala			
420	425	430	
cat aac ctg aca gca tat tgc tac cga ttc aac acc aag aca gac gat			1344
His Asn Leu Thr Ala Tyr Cys Tyr Arg Phe Asn Thr Lys Thr Asp Asp			
435	440	445	
tac aac agg gaa gaa ggc gtg gcg cat ttc tcg gac gtg atc ttc atc			1392

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 450 455 460
 ttc aac aac ctt aat ggt tat ggg ttc agt ccg aac ccg ttc acc aat 1440
 Phe Asn Asn Leu Asn Gly Tyr Gly Phe Ser Pro Asn Pro Phe Thr Asn
 465 470 475 480
 gct cca gag agc tat act gag ctt agc tac ctc atg tcc ggc tcg tgg 1488
 Ala Pro Glu Ser Tyr Thr Glu Leu Ser Tyr Leu Met Ser Gly Ser Trp
 485 490 495
 atc agc ttc act aat agt ctg gat cct aat aag tgg act ggt cgc gga 1536
 Ile Ser Phe Thr Asn Ser Leu Asp Pro Asn Lys Trp Thr Gly Arg Gly
 500 505 510
 agg aac gct acg aag acg gag aat tgg ccc gtg tat gat ctg gag aat 1584
 Arg Asn Ala Thr Lys Thr Glu Asn Trp Pro Val Tyr Asp Leu Glu Asn
 515 520 525
 ccc ttg agt atg atc tgg gat gcg aat gtc act tcg tat gcg gcg ccg 1632
 Pro Leu Ser Met Ile Trp Asp Ala Asn Val Thr Ser Tyr Ala Ala Pro
 530 535 540
 gat act tgg cgt aag gag ggt att gcg ttg att aat gct aat cgg agg 1680
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<210> 33

<211> 564

<212> PRT

<213> *Aspergillus niger*

<400> 33

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 35 40 45
 Ile Pro Phe Ala Lys Pro Pro Leu Ala His Leu Arg Trp Ala Asn Pro
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 Glu Ser Leu Asn Glu Ser Trp Ser Gly Leu Arg Pro Ala Thr Gly Tyr
 65 70 75 80
 Ala Met Glu Cys Ile Gly Tyr Gly Ser Asp Gln Lys Gly Tyr Leu Gln
 85 90 95
 Ser Glu Asp Cys Leu Tyr Leu Asn Val Arg Pro Ala Glu Tyr Asp
 100 105 110

21078WO.ST25.txt

Asn Ala Ser Leu Pro Val Leu Val Trp Ile His Gly Gly Gly Phe Ala
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 Gln Gly Gly Thr Pro Asp Leu Arg Tyr Asn Leu Thr Phe Ile Val Glu
 130 135 140
 His Ser Val Asn Ile Gly Gln Pro Ile Ile Ala Val Ser Val Ala Tyr
 145 150 155 160
 Arg Leu Gly Pro Trp Gly Phe Phe Asn Gly Val Glu Leu Ala Asn Glu
 165 170 175
 Gly Ser Leu Asn Leu Gly Leu Lys Asp Gln Arg Leu Ala Leu His Trp
 180 185 190
 Val Lys Glu Asn Ile Ala Gly Phe Gly Gly Asp Pro Ser Lys Val Val
 195 200 205
 Ile Tyr Gly Gln Ser Ala Gly Ser Glu Ser Val Gly Tyr Gln Ile Arg
 210 215 220
 Ala Tyr Asn Gly Arg Asp Asp Gly Leu Phe Arg Gly Gly Met Met Glu
 225 230 235 240
 Ser Gly Ala Val Leu Pro Gly Ser Ala Leu Asn Leu Thr Trp Thr Tyr
 245 250 255
 Glu Pro Trp Phe Gln Gln Ile Ala Asp Glu Ala Gly Cys Ser Gln Thr
 260 265 270
 Thr Arg Lys Leu Asp Cys Leu Arg Arg Thr Pro Phe Thr Val Leu Asn
 275 280 285
 Asn Ile Leu Asn Thr Thr Ala Asn Asp Thr Thr Pro Tyr Asn Trp Arg
 290 295 300
 Pro Thr Val Asp Gly Asp Phe Val Ala Arg Tyr Pro Ser Glu Gln Leu
 305 310 315 320
 Asp Thr Gly Asp Phe Val Lys Val Pro Ile Ile Ile Gly Tyr Thr Thr
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 Asp Glu Gly Thr Thr Glu Cys Pro Glu Pro Val Asn Thr Thr Ala Glu
 340 345 350
 Leu Lys Glu Tyr Leu Ser Ser Thr Thr Thr Tyr Gly Trp Ala Leu Asp
 355 360 365
 Ser Gln Val Val Ser Ser Leu Leu Asp Leu Tyr Pro Asn Thr Thr Ser
 370 375 380
 Phe Gly Ile Pro Ser Ser Glu Glu Leu Gly Gly Asn Val Thr Phe Pro
 385 390 395 400
 Gln Pro Tyr Gly Ala Ala Phe Arg Gln Thr Ala Ala Tyr Tyr Gly Asp
 405 410 415
 Ala Gln Phe Ile Ala Ala Thr Arg Tyr Thr Cys Glu Leu Trp Ala Ala
 420 425 430
 His Asn Leu Thr Ala Tyr Cys Tyr Arg Phe Asn Thr Lys Thr Asp Asp
 435 440 445
 Tyr Asn Arg Glu Glu Gly Val Ala His Phe Ser Asp Val Ile Phe Ile
 450 455 460

21078W0.ST25.txt

Phe Asn Asn Leu Asn Gly Tyr Gly Phe Ser Pro Asn Pro Phe Thr Asn
 465 470 475 480
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 485 490 495
 Ile Ser Phe Thr Asn Ser Leu Asp Pro Asn Lys Trp Thr Gly Arg Gly
 500 505 510
 Arg Asn Ala Thr Lys Thr Glu Asn Trp Pro Val Tyr Asp Leu Glu Asn
 515 520 525
 Pro Leu Ser Met Ile Trp Asp Ala Asn Val Thr Ser Tyr Ala Ala Pro
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 Asp Thr Trp Arg Lys Glu Gly Ile Ala Leu Ile Asn Ala Asn Arg Arg
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<210> 34

<211> 2371

<212> DNA

<213> *Aspergillus niger*

<400> 34

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ggggcgacgg cagctacggc tcacaaattg tgatggaata gacacggcat gatgtttcaa 180
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21078W0.ST25.txt

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<210> 35

<211> 789

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(789)

<400> 35

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gcc ctt tcc acc cca ctg gca acc gac gcc gaa aac ctc tac gca cgt	96
Ala Leu Ser Thr Pro Leu Ala Thr Asp Ala Glu Asn Leu Tyr Ala Arg	
20 25 30	
caa ttc ggc acg ggc tct aca gcc aac gaa ctc gag cag gga agc tgc	144
Gln Phe Gly Thr Gly Ser Thr Ala Asn Glu Leu Glu Gln Gly Ser Cys	
35 40 45	
aag gat gtg act ctc atc ttt gcg agg ggg tca act gag ctt ggg aat	192
Lys Asp Val Thr Leu Ile Phe Ala Arg Gly Ser Thr Glu Leu Gly Asn	
50 55 60	
atg ggc acc gta atc ggc ccc cct ctc tgc gac aac ctg aaa tcc aaa	240
Met Gly Thr Val Ile Gly Pro Pro Leu Cys Asp Asn Leu Lys Ser Lys	
65 70 75 80	

21078W0.ST25.txt

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      85                      90                      95
gcc gga ctc gtg cag aat gcc ctg ccc cag aac acc gat ccg ggg agt      336
Ala Gly Leu Val Gln Asn Ala Leu Pro Gln Asn Thr Asp Pro Gly Ser
      100                     105                     110
atc tcc gcc gcg aag cag atg ttc gag gag gcg aat tcg aag tgt ccc      384
Ile Ser Ala Ala Lys Gln Met Phe Glu Glu Ala Asn Ser Lys Cys Pro
      115                     120                     125
aat act aag att gtt gcg ggt ggt tat agt caa gga agc gct gtg att      432
Asn Thr Lys Ile Val Ala Gly Gly Tyr Ser Gln Gly Ser Ala Val Ile
      130                     135                     140
gac aac gcc gtg caa gaa ctc agc acc acc gtg aaa gac caa gtg aag      480
Asp Asn Ala Val Gln Glu Leu Ser Thr Thr Val Lys Asp Gln Val Lys
      145                     150                     155                     160
ggg gtc gtg ctc ttc ggg ttc acg aga aac gtg cag gat cac ggg cag      528
Gly Val Val Leu Phe Gly Phe Thr Arg Asn Val Gln Asp His Gly Gln
      165                     170                     175
atc cct aat tac cct aag gat gac gtg aag gtt tat tgt gcc gtg ggc      576
Ile Pro Asn Tyr Pro Lys Asp Asp Val Lys Val Tyr Cys Ala Val Gly
      180                     185                     190
gat ctg gtc tgt gat gat acg ttg gtt gtt acg gcg atg cat ctg acg      624
Asp Leu Val Cys Asp Asp Thr Leu Val Val Thr Ala Met His Leu Thr
      195                     200                     205
tat ggc atg gat gcg ggt gat gcg gcg agc ttt ttg gcc gag aag gtg      672
Tyr Gly Met Asp Ala Gly Asp Ala Ala Ser Phe Leu Ala Glu Lys Val
      210                     215                     220
cag tct tcc agt agt tcg act act agc tcc agc tcg gat gcc gcg agt      720
Gln Ser Ser Ser Ser Ser Thr Thr Ser Ser Ser Ser Asp Ala Ala Ser
      225                     230                     235                     240
agt tca tct gct gcg ggg acg tcg tcg tcg ggg ttg tcg gga ctg tct      768
Ser Ser Ser Ala Ala Gly Thr Ser Ser Ser Gly Leu Ser Gly Leu Ser
      245                     250                     255
tct ttt ttt gga ggt ctc taa      789
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<210> 36

<211> 262

<212> PRT

<213> Aspergillus niger

<400> 36

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 35 40 45
 Lys Asp Val Thr Leu Ile Phe Ala Arg Gly Ser Thr Glu Leu Gly Asn
 50 55 60
 Met Gly Thr Val Ile Gly Pro Pro Leu Cys Asp Asn Leu Lys Ser Lys
 65 70 75 80
 Leu Gly Ser Asp Lys Val Ala Cys Gln Gly Val Gly Gly Gln Tyr Ser
 85 90 95
 Ala Gly Leu Val Gln Asn Ala Leu Pro Gln Asn Thr Asp Pro Gly Ser
 100 105 110
 Ile Ser Ala Ala Lys Gln Met Phe Glu Glu Ala Asn Ser Lys Cys Pro
 115 120 125
 Asn Thr Lys Ile Val Ala Gly Gly Tyr Ser Gln Gly Ser Ala Val Ile
 130 135 140
 Asp Asn Ala Val Gln Glu Leu Ser Thr Thr Val Lys Asp Gln Val Lys
 145 150 155 160
 Gly Val Val Leu Phe Gly Phe Thr Arg Asn Val Gln Asp His Gly Gln
 165 170 175
 Ile Pro Asn Tyr Pro Lys Asp Asp Val Lys Val Tyr Cys Ala Val Gly
 180 185 190
 Asp Leu Val Cys Asp Asp Thr Leu Val Val Thr Ala Met His Leu Thr
 195 200 205
 Tyr Gly Met Asp Ala Gly Asp Ala Ala Ser Phe Leu Ala Glu Lys Val
 210 215 220
 Gln Ser Ser Ser Ser Ser Thr Thr Ser Ser Ser Ser Asp Ala Ala Ser
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 245 250 255
 Ser Phe Phe Gly Gly Leu
 260

<210> 37

<211> 2981

<212> DNA

<213> *Aspergillus niger*

<400> 37

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21078WO.ST25.txt

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cgagtcctac	gtacagctaa	gcaacttgat	gaccagcatg	tgggcaccc	tcacccacga	1920
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tcagccggtt	gatctagtgt	ttgatgcgaa	tgtcacgagc	tacagctaca	tggagccaga	2040
cacgtggcgg	aaggagggga	tcgactatat	caattccgtg	gccaacgcgt	actggcgata	2100
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cgaaaggaac taaaccaata ctaagaaaaa aaaaaaagag taaagaaaaa agagtaaaaa	2880
accaagctcg gaaagtaaaa atttcccctg gtcttgttgt cattccccta cctattgaga	2940
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<212> DNA

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<220>

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1 5 10 15	
gca gcg cca acc aaa gtg gcc cgt tcc acg gcc agt cct acg gcc aag	96
Ala Ala Pro Thr Lys Val Ala Arg Ser Thr Ala Ser Pro Thr Ala Lys	
20 25 30	
gtt cgc aac ggt aca tat gtc gga gtg aca aat gcg cat tac cag caa	144
Val Arg Asn Gly Thr Tyr Val Gly Val Thr Asn Ala His Tyr Gln Gln	
35 40 45	
gat ttc ttt ttg gga atg ccg tat gcc cag cag cct tta ggt gac ttg	192
Asp Phe Phe Leu Gly Met Pro Tyr Ala Gln Gln Pro Leu Gly Asp Leu	
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cgc ttc acg gtg cct cag tcc ctg aac gaa agc tgg agt ggc gag cgc	240
Arg Phe Thr Val Pro Gln Ser Leu Asn Glu Ser Trp Ser Gly Glu Arg	
65 70 75 80	
gac gcg aag gaa tat tcc aat atc tgt gta gga tac ggt acc gac tcg	288
Asp Ala Lys Glu Tyr Ser Asn Ile Cys Val Gly Tyr Gly Thr Asp Ser	
85 90 95	
att tgg tac cca cag tcc gaa gct tgt cta acc ttg aat gtc atc cgc	336
Ile Trp Tyr Pro Gln Ser Glu Ala Cys Leu Thr Leu Asn Val Ile Arg	
100 105 110	
gat tct tct gca aat gag aac tcg aag ctc ccc gtg ggc gtc tgg ata	384
Asp Ser Ser Ala Asn Glu Asn Ser Lys Leu Pro Val Gly Val Trp Ile	
115 120 125	
cat gga ggt ggc ttc ttt gag gga tct agt gct gac cag cgc tac aac	432
His Gly Gly Gly Phe Phe Glu Gly Ser Ser Ala Asp Gln Arg Tyr Asn	
130 135 140	
atg tcc gcg att gtt gcc aac tcc tat aag atc gga aag ccg ttc att	480

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Met Ser Ala Ile Val Ala Asn Ser Tyr Lys Ile Gly Lys Pro Phe Ile	
145 150 155 160	
gct gtc agc tta aac tat cgc ctt tcg gca tgg ggc ttc ttg agt tcc	528
Ala Val Ser Leu Asn Tyr Arg Leu Ser Ala Trp Gly Phe Leu Ser Ser	
165 170 175	
agt caa gtc tgg ggc act ggc aat acc aat cta ggt atc agg gat caa	576
Ser Gln Val Trp Gly Thr Gly Asn Thr Asn Leu Gly Ile Arg Asp Gln	
180 185 190	
agg tta gca ctc cat tgg atc aag gag aat atc gcg gca ttc gga gga	624
Arg Leu Ala Leu His Trp Ile Lys Glu Asn Ile Ala Ala Phe Gly Gly	
195 200 205	
gac cca gat aag atc act atc tgg ggc gaa tct gcc gga gcg atg tcc	672
Asp Pro Asp Lys Ile Thr Ile Trp Gly Glu Ser Ala Gly Ala Met Ser	
210 215 220	
gtg ggt tat cac ctt gca gca tac ggc ggt agg gac gat gga ctc ttc	720
Val Gly Tyr His Leu Ala Ala Tyr Gly Gly Arg Asp Asp Gly Leu Phe	
225 230 235 240	
cgt gga gga att atg gag tca gga ggg act att gca gct agt cca gcc	768
Arg Gly Gly Ile Met Glu Ser Gly Gly Thr Ile Ala Ala Ser Pro Ala	
245 250 255	
aac tat acc ggg tac caa gcg cac tat gat gag ctc gcg ggt caa gtc	816
Asn Tyr Thr Gly Tyr Gln Ala His Tyr Asp Glu Leu Ala Gly Gln Val	
260 265 270	
ggt tgc tcc gac gta gta gat tcg ttg cag tgc ctg cgc gaa gtt ccg	864
Gly Cys Ser Asp Val Val Asp Ser Leu Gln Cys Leu Arg Glu Val Pro	
275 280 285	
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Phe Glu Lys Leu Asn Ala Ala Leu Asn Thr Thr Ser Gly Asn Ser Asp	
290 295 300	
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Phe Asn Phe Gly Pro Val Ile Asp Gly Asp Ile Ile Arg Asp Trp Gly	
305 310 315 320	
agc ctc cag cta gac aag cat gaa ttc gtc aaa gtc cct att ctt gca	1008
Ser Leu Gln Leu Asp Lys His Glu Phe Val Lys Val Pro Ile Leu Ala	
325 330 335	
ggt acc aat acc gac gaa ggg aca gcc ttt ggg ccc aca ggt atc aac	1056
Gly Thr Asn Thr Asp Glu Gly Thr Ala Phe Gly Pro Thr Gly Ile Asn	
340 345 350	
acg aca gag gag ttc tat gca tat ctc aca gat ggc gaa tct gga ttc	1104
Thr Thr Glu Glu Phe Tyr Ala Tyr Leu Thr Asp Gly Glu Ser Gly Phe	
355 360 365	
cag cta ccc ccc acg atc gcc cag gaa atc ctg cag ctc tac cct gat	1152
Gln Leu Pro Pro Thr Ile Ala Gln Glu Ile Leu Gln Leu Tyr Pro Asp	
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tcc aaa ggc tac caa tgg cgg cgc acc tgt gca tac gca ggg gac tat      1248
Ser Lys Gly Tyr Gln Trp Arg Arg Thr Cys Ala Tyr Ala Gly Asp Tyr
          405          410          415
gta atg cat gcc aac cgt cgc cga caa tgt gag gcg tgg aca gag acc      1296
Val Met His Ala Asn Arg Arg Arg Gln Cys Glu Ala Trp Thr Glu Thr
          420          425          430
tcg acg acg gcg tac tgt tat cga ttc aat atg cgt gcg gcc gat gtc      1344
Ser Thr Thr Ala Tyr Cys Tyr Arg Phe Asn Met Arg Ala Ala Asp Val
          435          440          445
ccc atc ctg tct ggc gcc acc cat ttt gaa gaa gtt gct ttt gta ttc      1392
Pro Ile Leu Ser Gly Ala Thr His Phe Glu Glu Val Ala Phe Val Phe
          450          455          460
aac aac att gca gga ctc ggg tac cat tac gga aag ccg ttc gca ggg      1440
Asn Asn Ile Ala Gly Leu Gly Tyr His Tyr Gly Lys Pro Phe Ala Gly
465          470          475          480
atg ccc gag tcc tac gta cag cta agc aac ttg atg acc agc atg tgg      1488
Met Pro Glu Ser Tyr Val Gln Leu Ser Asn Leu Met Thr Ser Met Trp
          485          490          495
gca tcc ttc atc cac gat tta gac cct aat tcg ggc atc aag gac tca      1536
Ala Ser Phe Ile His Asp Leu Asp Pro Asn Ser Gly Ile Lys Asp Ser
          500          505          510
gct gta cag tgg caa ccg tac ggg aag gat cag ccg gtt gat cta gtg      1584
Ala Val Gln Trp Gln Pro Tyr Gly Lys Asp Gln Pro Val Asp Leu Val
          515          520          525
ttt gat gcg aat gtc acg agc tac agc tac atg gag cca gac acg tgg      1632
Phe Asp Ala Asn Val Thr Ser Tyr Ser Tyr Met Glu Pro Asp Thr Trp
          530          535          540
cgg aag gag ggg atc gac tat atc aat tcc gtg gcc aac gcg tac tgg      1680
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cga taa
Arg
1686

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<210> 39

<211> 561

<212> PRT

<213> *Aspergillus niger*

<400> 39

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50	55	60	
Arg Phe Thr Val Pro Gln Ser Leu Asn Glu Ser Trp Ser Gly Glu Arg			
65	70	75	80
Asp Ala Lys Glu Tyr Ser Asn Ile Cys Val Gly Tyr Gly Thr Asp Ser			
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100	105	110	
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130	135	140	
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Ala Val Ser Leu Asn Tyr Arg Leu Ser Ala Trp Gly Phe Leu Ser Ser			
165	170	175	
Ser Gln Val Trp Gly Thr Gly Asn Thr Asn Leu Gly Ile Arg Asp Gln			
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Arg Leu Ala Leu His Trp Ile Lys Glu Asn Ile Ala Ala Phe Gly Gly			
195	200	205	
Asp Pro Asp Lys Ile Thr Ile Trp Gly Glu Ser Ala Gly Ala Met Ser			
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Val Gly Tyr His Leu Ala Ala Tyr Gly Gly Arg Asp Asp Gly Leu Phe			
225	230	235	240
Arg Gly Gly Ile Met Glu Ser Gly Gly Thr Ile Ala Ala Ser Pro Ala			
245	250	255	
Asn Tyr Thr Gly Tyr Gln Ala His Tyr Asp Glu Leu Ala Gly Gln Val			
260	265	270	
Gly Cys Ser Asp Val Val Asp Ser Leu Gln Cys Leu Arg Glu Val Pro			
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Phe Glu Lys Leu Asn Ala Ala Leu Asn Thr Thr Ser Gly Asn Ser Asp			
290	295	300	
Phe Asn Phe Gly Pro Val Ile Asp Gly Asp Ile Ile Arg Asp Trp Gly			
305	310	315	320
Ser Leu Gln Leu Asp Lys His Glu Phe Val Lys Val Pro Ile Leu Ala			
325	330	335	
Gly Thr Asn Thr Asp Glu Gly Thr Ala Phe Gly Pro Thr Gly Ile Asn			
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Thr Thr Glu Glu Phe Tyr Ala Tyr Leu Thr Asp Gly Glu Ser Gly Phe			

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355	360	365
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370	375	380
Asp Pro Ala Leu Gly Ile Pro	Glu Phe Leu Gly Asp Thr Arg Val	Pro
385	390	395
Ser Lys Gly Tyr Gln Trp Arg Arg	Thr Cys Ala Tyr Ala Gly Asp Tyr	
405	410	415
Val Met His Ala Asn Arg Arg Arg	Gln Cys Glu Ala Trp Thr Glu Thr	
420	425	430
Ser Thr Thr Ala Tyr Cys Tyr Arg	Phe Asn Met Arg Ala Ala Asp Val	
435	440	445
Pro Ile Leu Ser Gly Ala Thr His	Phe Glu Glu Val Ala Phe Val Phe	
450	455	460
Asn Asn Ile Ala Gly Leu Gly Tyr His	Tyr Gly Lys Pro Phe Ala Gly	
465	470	475
Met Pro Glu Ser Tyr Val Gln Leu Ser	Asn Leu Met Thr Ser Met Trp	
485	490	495
Ala Ser Phe Ile His Asp Leu Asp	Pro Asn Ser Gly Ile Lys Asp Ser	
500	505	510
Ala Val Gln Trp Gln Pro Tyr Gly	Lys Asp Gln Pro Val Asp Leu Val	
515	520	525
Phe Asp Ala Asn Val Thr Ser Tyr	Ser Tyr Met Glu Pro Asp Thr Trp	
530	535	540
Arg Lys Glu Gly Ile Asp Tyr Ile	Asn Ser Val Ala Asn Ala Tyr Trp	
545	550	555
Arg		560